SUPPORTING INFORMATION

INTERPRETING PROTEIN STRUCTURAL DYNAMICS FROM NMR CHEMICAL SHIFTS

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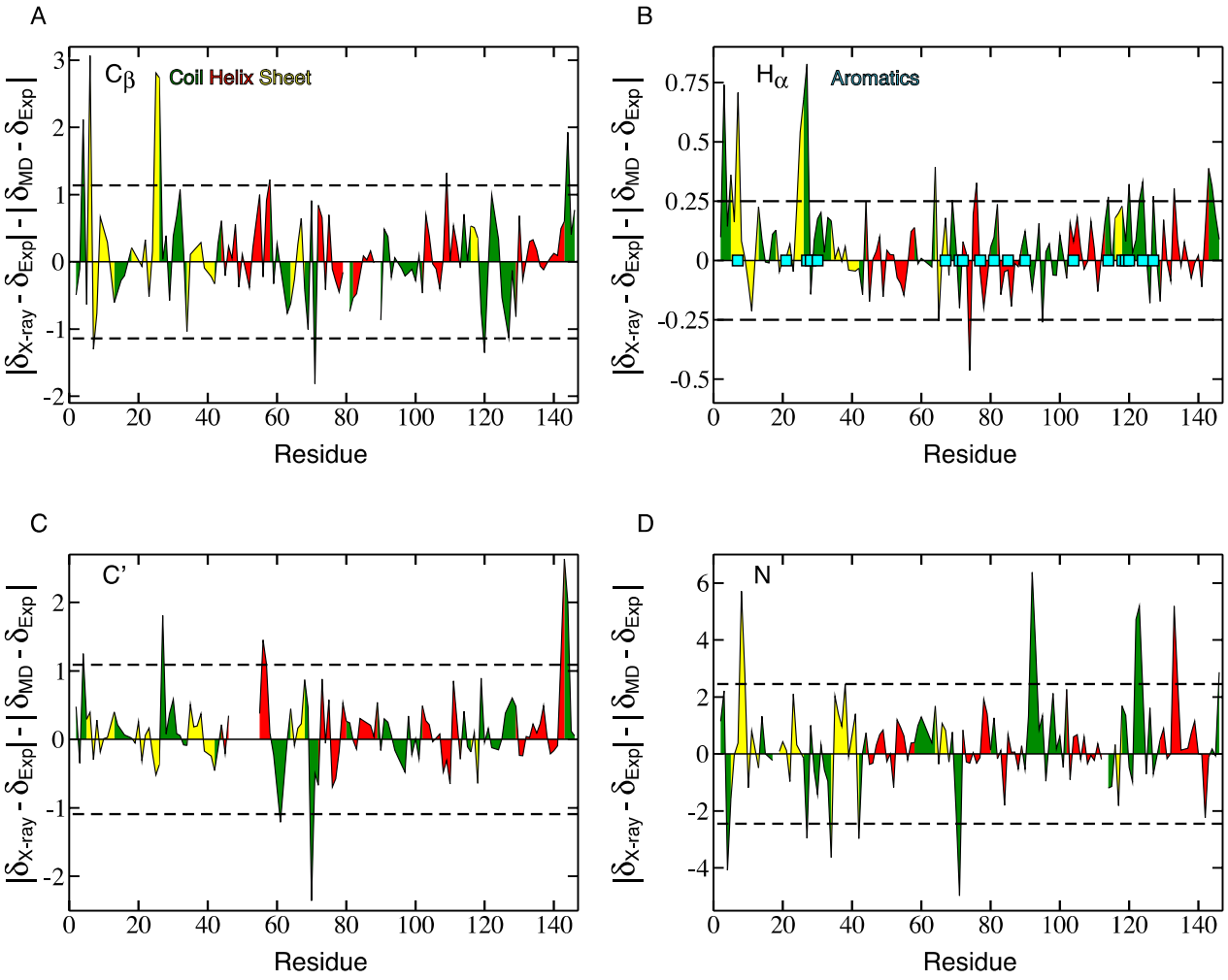

Figure S1. Comparison of Sparta+ chemical shift predictions for ttRNH obtained from an X-ray structure and a 100 ns MD simulation in the amber99SB force field. For each residue for which an experimentally measured chemical shift (δExp) was available, the magnitude of the deviation between the X-ray predicted value (δX-ray) and the experimental value, | δX-ray - δExp |, and the magnitude of the deviation between the MD averaged prediction (δMD) and the experimental value, | δMD - δExp |, are compared. |δX-ray - δExp| - | δMD - δExp | is shown for is shown for Cβ atoms in A, Hα atoms in B, C' atoms in C, and N atoms in D. Residues are colored according to their secondary structure in the X-ray structure with green, red, and yellow corresponding to coil, helix, and sheet respectively. Residues with aromatic side chains are displayed as cyan squares in B. The reported standard deviation of Sparta+ predictions obtained from a benchmark database of X-ray structures is displayed for each atom type as a dotted line for comparison

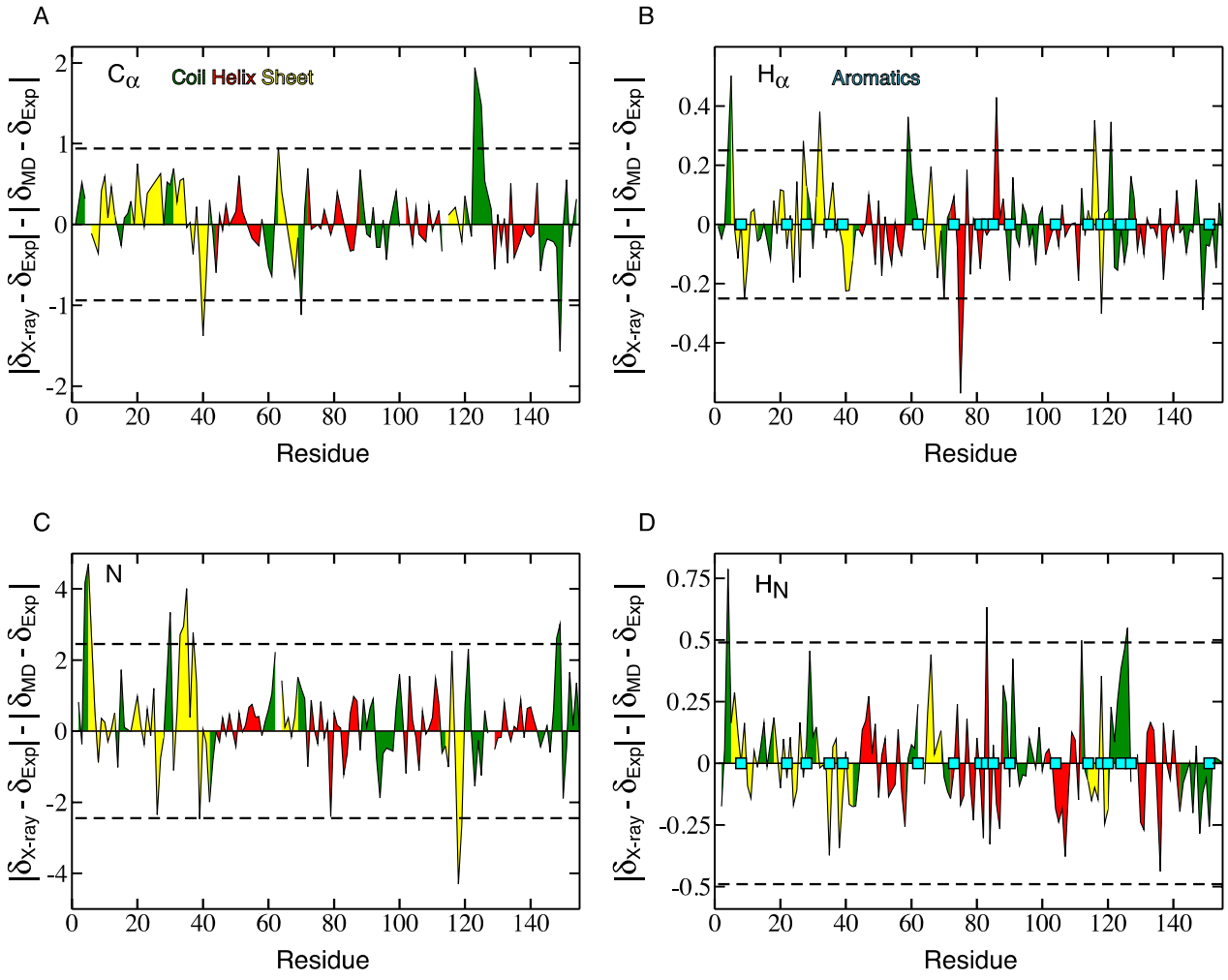

Figure S2. Comparison of Sparta+ chemical shift predictions for ecRNH obtained from an X-ray structure and a 100 ns MD simulation in the amber99SB force field. For each residue for which an experimentally measured chemical shift (δExp) was available, the magnitude of the deviation between the X-ray predicted value (δX-ray) and the experimental value, | δX-ray - δExp |, and the magnitude of the deviation between the MD averaged prediction (δMD) and the experimental value, | δMD - δExp |, are compared. |δX-ray - δExp| - | δMD - δExp | is shown for is shown for Cα atoms in A, Hα atoms in B, N atoms in C, and H_N atoms D. Residues are colored according to their secondary structure in the X-ray structure with green, red, and yellow corresponding to coil, helix, and sheet respectively. Residues with aromatic side chains are displayed as cyan squares in B and D. The reported standard deviation of Sparta+ predictions obtained from a benchmark database of X-ray structures is displayed for each atom type as a dotted line for comparison

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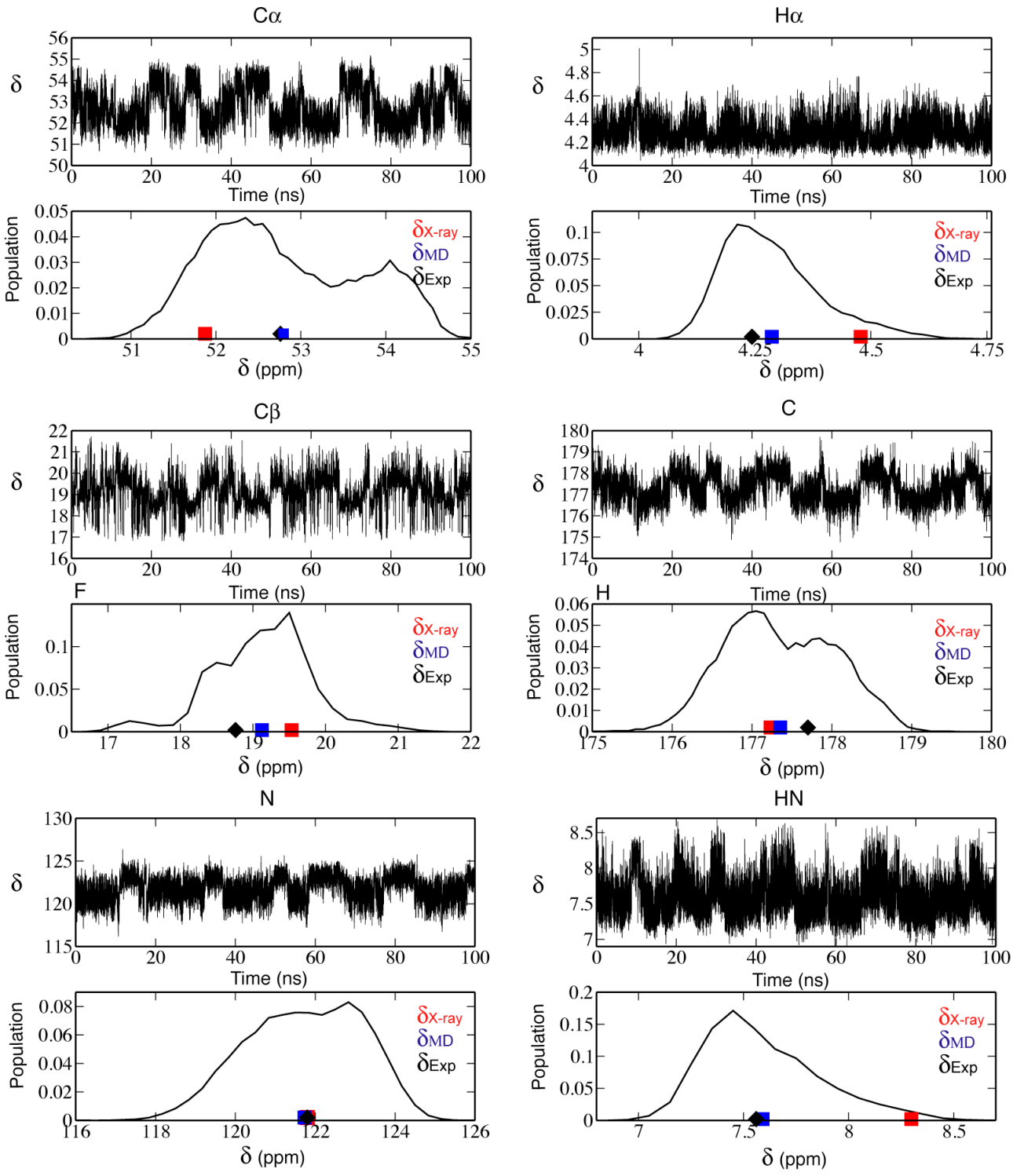

Figure S3. Chemical shift predictions of Ala 145 backbone shifts in a 100 ns MD simulation of ttRNH in the amber99SB force field. For each shift type, the value of the Sparta+ predicted chemical shift for snapshots saved every 4.5ps of the MD trajectory are shown in the top panel and the normalized distribution of the predicted shifts are shown in the bottom panel. The Sparta+ predictions obtained from the X-ray structure (pdb code 1RIL) are shown as red squares, the average value of the Sparta+ predictions over the entire MD trajectory are shown as blue squares, and the experimentally measured values shown as black diamonds.

SI Table 1. Comparison of Sparta+ Prediction RMSDs for multiple ttRNH MD simulations.

	SPARTA+ Prediction RMSD					
	Cα	Cβ	C'	HN	Hα	N
Amber99SB (100 ns)	0.68	1.01	1.06	0.35	0.23	2.17
Amber99SB-ILDN (450 ns)	0.72	1.02	1.08	0.37	0.24	2.06
Amber99SB (1 μs)	0.70	1.01	1.06	0.35	0.25	1.99

Comparison of MD averaged Sparta+ prediction RMSDs from experimental values for MD simulations of ttRNH of different lengths and in different force fields.

SI Table 2. Comparison of Sparta+ Prediction RMSDs for multiple ecRNH MD simulations.

	SPARTA+ Prediction RMSD			
	Cα	HN	Hα	N
Amber99SB (100 ns)	0.70	0.36	0.25	2.25
Amber99SB-ILDN (450 ns)	0.74	0.36	0.25	2.29
Amber99SB (1 μs)	0.75	0.36	0.27	2.32

Comparison of MD averaged Sparta+ prediction RMSDs from experimental values for MD simulations of ecRNH of different lengths and in different force fields.

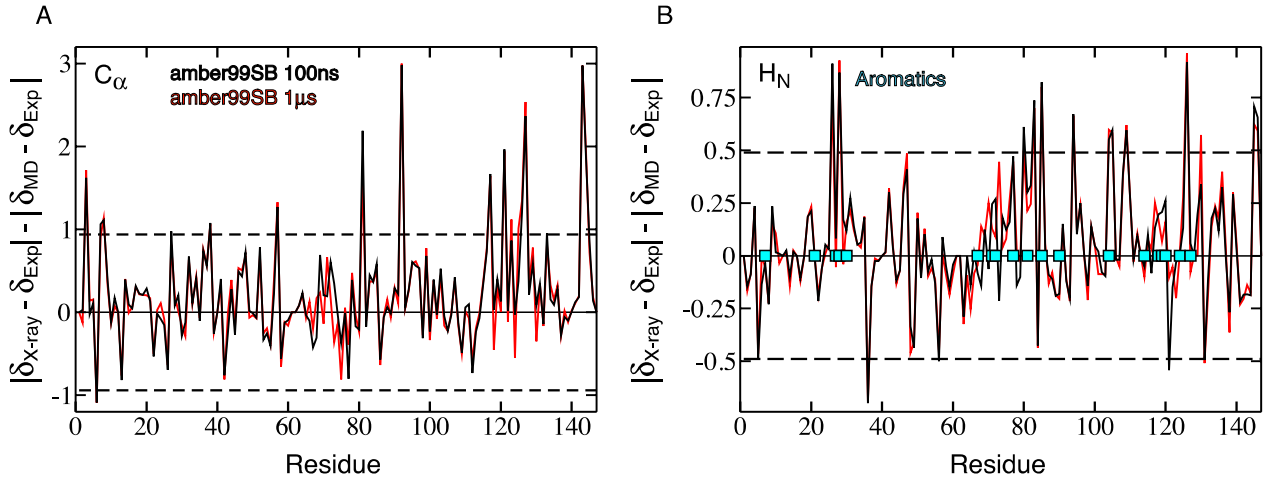

Figure S4. Comparison of Sparta+ chemical shift predictions for a 100 ns and a 1 μs MD simulation of ttRNH in the amber99SB force field. For each residue for which an experimentally measured chemical shift (δExp) was available, the magnitude of the deviation between the X-ray predicted value (δX-ray) and the experimental value, | δX-ray - δExp |, and the magnitude of the deviation between the MD averaged prediction (δMD) and the experimental value, | δMD - δExp |, are compared. |δX-ray - δExp| - | δMD - δExp | is shown for Cα atoms in A and HN atoms in B. Values obtained from a 100 ns simulation shown in black, and values obtained from a 1 μs simulation are shown in red. Residues with aromatic side chains are displayed as cyan squares in B. The reported standard deviation

of Sparta+ predictions obtained from a benchmark database of X-ray structures is displayed for each atom type as a dotted line for comparison.

SI Table 3. Comparison of Chemical Shift Prediction RMSDs for multiple Chemical Shift Prediction Progorams for a 100ns MD simulation of ttRNH in the amber99SB force field.

	Cα			Cβ			C'			HN			Hα			N		
	X-ray	MD	Ratio	X-ray	MD	Ratio	X-ray	MD	Ratio	X-ray	MD	Ratio	X-ray	MD	Ratio	X-ray	MD	Ratio
ShiftS	1.35	0.87	0.64	1.56	1.21	0.76	1.89	1.31	0.69	0.64	0.56	0.88	-	-	-	4.89	3.72	0.76
CamShift	1.18	0.88	0.75	1.51	1.21	0.80	1.32	1.21	0.92	0.54	0.42	0.78	0.34	0.23	0.68	3.32	2.65	0.79
SPARTA+	1.00	0.68	0.68	1.14	1.01	0.89	1.21	1.06	0.88	0.44	0.35	0.79	0.32	0.23	0.72	2.70	2.17	0.80
SHIFTX+	0.94	0.68	0.72	1.24	1.04	0.84	1.34	1.08	0.80	0.44	0.32	0.73	0.30	0.19	0.63	2.82	2.15	0.76
SHIFTX2	0.84	0.68	0.81	1.24	1.04	0.84	1.34	1.08	0.80	0.42	0.32	0.76	0.30	0.19	0.63	3.04	2.30	0.76

Comparison of RMSDs between experimental chemical shifts and Sparta+ chemical shift predictions obtained from an X-ray structure (PDB code 1RIL) and an unbiased 100ns MD Simulation using the amber99SB force field using several different chemical shift prediction software tools. The ratio of RMSDs values (MD RMSD / X-ray RMSD) is also shown for each atom type for each predictor.

SI Table 4. Comparison of Chemical Shift Prediction RMSDs for multiple Chemical Shift Prediction Progorams for a 100ns MD simulation of ecRNH in the amber99SB force field.

	Cα			HN			Hα			N		
	X-ray	MD	Ratio	X-ray	MD	Ratio	X-ray	MD	Ratio	X-ray	MD	Ratio
ShiftS	1.02	0.90	0.88	0.70	0 .69	0.98	-	-	-	3.75	3.82	1.02
CamShift	0.99	0.92	0.93	0.45	0.42	0.93	0.25	0.27	1.08	3.02	2.92	0.96
SPARTA+	0.74	0.70	0.95	0.39	0.36	0.92	0.25	0.25	1.00	2.51	2.25	0.90
SHIFTX+	0.64	0.71	1.05	0.37	0.39	1.05	0.19	0.22	1.15	2.18	2.27	1.04
SHIFTX2	0.44	0.36	0.81	0.22	0.27	1.23	0.09	0.15	1.66	2.17	1.59	0.73

Comparison of RMSDs between experimental chemical shifts and Sparta+ chemical shift predictions obtained from an X-ray structure (PDB code 2RN2) and an unbiased 100ns MD Simulation using the amber99SB force field using several different chemical shift prediction software tools. The ratio of RMSDs values (MD RMSD / X-ray RMSD) is also shown for each atom type for each predictor.

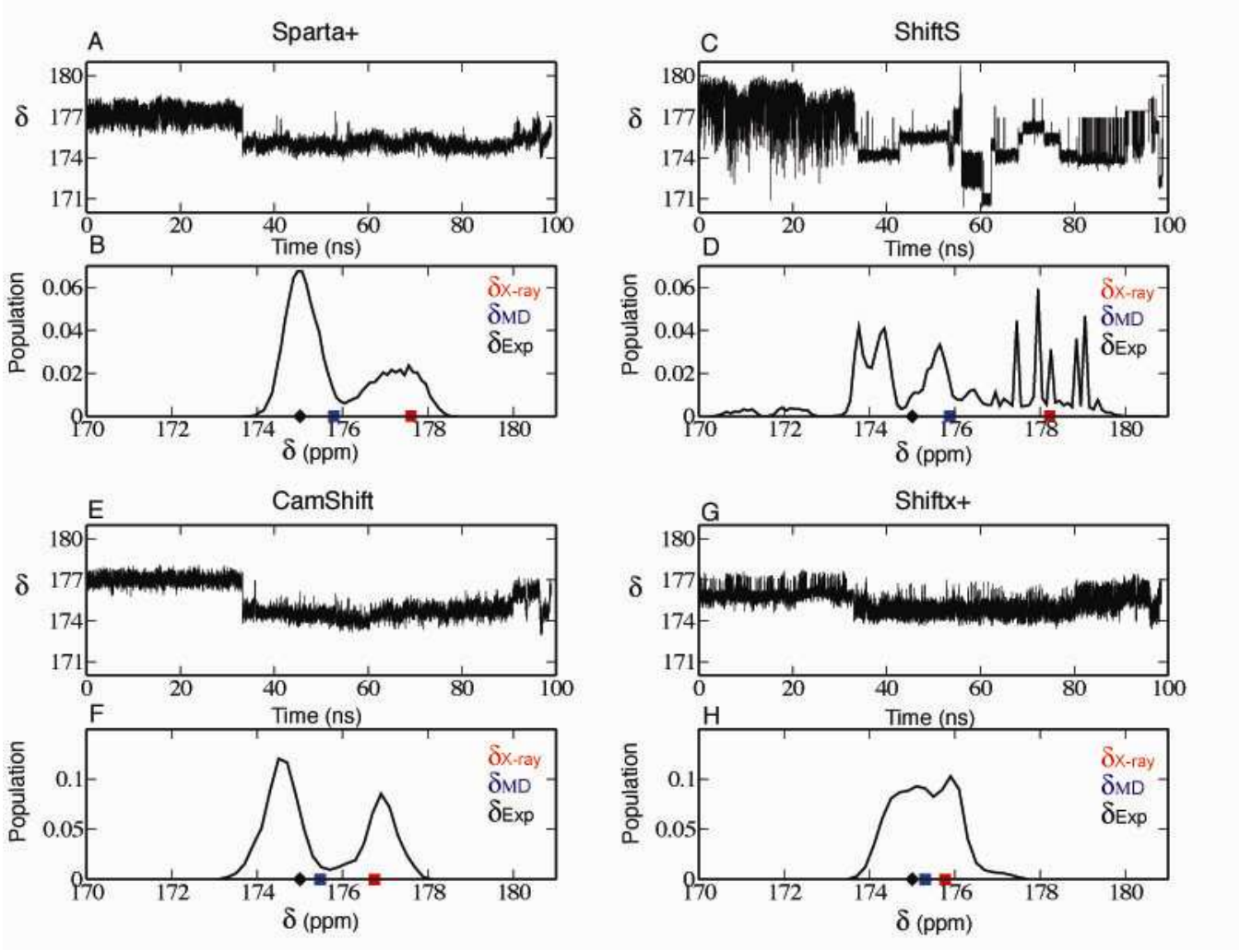

Figure S5. Chemical shift predictions of Phe 27 C' in a 100 ns MD simulation of ttRNH in the amber99SB force field. A) The value of the Sparta+ predicted chemical shift of Phe 27 C' for snapshots saved every 4.5ps of the MD trajectory. B) The normalized distribution of the Sparta+ predicted shifts of Phe 27 C' from the MD trajectory. C) The value of the ShiftS predicted chemical shift of Phe 27 C' for snapshots saved every 4.5ps of the MD trajectory. D) The normalized distribution of the ShiftS predicted shifts of Phe 27 C' from the MD trajectory E) The value of the CamShift predicted chemical shift of Phe 27 C' for snapshots saved every 4.5ps of the MD trajectory. F) The normalized distribution of the CamShift predicted shifts of Phe 27 C' from the MD trajectory. G) The value of the Shiftx+ predicted chemical shift of Phe 27 C' for snapshots saved every 4.5ps of the MD trajectory. H) The normalized distribution of the Shiftx+ predicted shifts of Phe 27 C' from the MD trajectory. For each shift predictor, the prediction obtained from the X-ray structure (pdb code 1RIL) is shown as a red square, the average value of the predictions over the entire MD trajectory is shown as a blue square, and the experimentally measured value is shown as a black diamond.